Amendments to the Specification:

Please replace the title of the invention with the following rewritten title:

--~~SYSTEMS AND METHODS FOR~~ <u>METHOD OF IMPUTING MISSING VALUES IN MICROARRAY DATA</u> ~~ANALYSIS~~--

Please replace the paragraph beginning at line 4 of page 24 with the following rewritten paragraph:

--Missing entries were created as follows: each entry in a complete matrix of available microarray data was randomly and independently marked as missing with a probability p. For each of the two data sets used, four missing probabilities were used to render different proportions of missing entries. As an example, the yeast cell cycle data~~, http://rana.lbl.gov/EisenData.htm,~~ (Eisen, et al. (1998) *Proc. Natl. Acad. Sci. USA* 95:14863-8) with 6221 genes (rows) and 80 experiments (columns) was used. The columns were correlated and some columns were replicated experiments. In the original data, each column had at least 182, and up to 765 missing entries. If a missing entry arises randomly and independently with probability p, then the expected number of genes with s missing entries is:

$$E_M = 6221 \binom{80}{s} p^s (1-p)^{80-s} . --$$